

T640X

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Godowski, Paul J.
Gurney, Austin L.

(ii) TITLE OF INVENTION: Tie Ligands

10 (iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

25 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

30 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger R.
(B) REGISTRATION NUMBER: 33,055
(C) REFERENCE/DOCKET NUMBER: P1130

35 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-3216

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2290 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCTGAGGGG AGGCCCGGAG CCTTTCTGGG GCCTGGGGGA TCCTCTTGCA 50

15 CTGGTGGGTG GAGAGAAGCG CCTGCAGCCA ACCAGGGTCA GGCTGTGCTC 100

ACAGTTTCCT CTGGCGGCAT GTAAAGGCTC CACAAAGGAG TTGGGAGTTC 150

20 AAATGAGGCT GCTGCGGACG GCCTGAGGAT GGACCCCAAG CCCTGGACCT 200

GCCGAGCGTG GCACTGAGGC AGCGGCTGAC GCTACTGTGA GGGAAAGAAG 250

GTTGTGAGCA GCCCCGCAGG ACCCCTGGCC AGCCCTGGCC CCAGCCTCTG 300

25 CCGGAGCCCT CTGTGGAGGC AGAGCCAGTG GAGCCCAGTG AGGCAGGGCT 350

GCTTGGCAGC CACCGGCCTG CAACTCAGGA ACCCCTCCAG AGGCCATGGA 400

30 CAGGCTGCC CGCTGACGGC CAGGGTGAAG CATGTGAGGA GCCGCCCGG 450

AGCCAAGCAG GAGGGAAGAG GCTTCATAG ATTCTATTCA CAAAGAATAA 500

CCACCATTTC GCAAGGACCA TGAGGCCACT GTGCGTGACA TGCTGGTGGC 550

35 TCGGACTGCT GGCTGCCATG GGAGCTGTTG CAGGCCAGGA GGACGGTTT 600

GAGGGCACTG AGGAGGGCTC GCCAAGAGAG TTCATTACCA TAAACAGGTA 650

PATENT DOCKET P1130

CAAGCGGGCG GGCAGTCCC AGGACAAGTG CACCTACACC TTCATTGTGC 700

CCCAGCAGCG GGTACGGGT GCCATCTGCG TCAACTCCAA GGAGCCTGAG 750

5 GTGCTTCTGG AGAACCGAGT GCATAAGCAG GAGCTAGAGC TGCTAACAA 800

TGAGCTGCTC AAGCAGAAGC GGCAGATCGA GACGCTGCAG CAGCTGGTGG 850

10 AGGTGGACGG CGGCATTGTG AGCGAGGTGA AGCTGCTGCG CAAGGAGAGC 900

CGCAACATGA ACTCGCGGGT CACGCAGCTC TACATGCAGC TCCTGCACGA 950

GATCATCCGC AAGCGGGACA ACGCGTTGGA GCTCTCCCAG CTGGAGAAC 1000

15 GGATCCTGAA CCAGACAGCC GACATGCTGC AGCTGGCCAG CAAGTACAAG 1050

GACCTGGAGC ACAAGTACCA GCACCTGGCC ACACTGGCCC ACAACCAATC 1100

AGAGATCATC GCGCAGCTTG AGGAGCACTG CCAGAGGGTG CCCTCGGCCA 1150

20 GGCCCCGTCCC CCAGCCACCC CCCGCTGCC CGCCCCGGGT CTACCAACCA 1200

CCCACCTACA ACCGCATCAT CAACCAGATC TCTACCAACG AGATCCAGAG 1250

25 TGACCAGAAC CTGAAGGTGC TGCCACCCCC TCTGCCCACT ATGCCCACTC 1300

TCACCAGCCT CCCATTTCC ACCGACAAGC CGTCGGGCC ATGGAGAGAC 1350

TGCCTGCAGG CCCTGGAGGA TGGCCACGAC ACCAGCTCCA TCTACCTGGT 1400

30 GAAGCCGGAG AACACCAACC GCCTCATGCA GGTGTGGTGC GACCAGAGAC 1450

ACGACCCCCGG GGGCTGGACC GTCATCCAGA GACGCCTGGA TGGCTCTGTT 1500

35 AACTTCTTCA GGAACCTGGGA GACGTACAAG CAAGGGTTTG GGAACATTGA 1550

CGGCGAATAC TGGCTGGGCC TGGAGAACAT TTACTGGCTG ACGAACCAAG 1600

PATENT DOCKET P1130

GCAACTACAA ACTCCTGGTG ACCATGGAGG ACTGGTCCGG CCGCAAAGTC 1650

TTTGCAGAAT ACGCCAGTTT CCGCCTGGAA CCTGAGAGCG AGTATTATAA 1700

5 GCTGCGGCTG GGGCGCTACC ATGGCAATGC GGGTGACTCC TTTACATGGC 1750

ACAACGGCAA GCAGTTCACCC ACCCTGGACA GAGATCATGA TGTCTACACA 1800

10 GGAAACTGTG CCCACTACCA GAAGGGAGGC TGGTGGTATA ACGCCTGTGC 1850

15 GCTACCAGGA CGGAGTCTAC TGGGCTGAGT TCCGAGGAGG CTCTTACTCA 1950

CTCAAGAAAG TGGTGATGAT GATCCGACCG AACCCCAACA CCTTCCACTA 2000

20 AGCCAGCTCC CCCTCCTGAC CTCTCGTGGC CATTGCCAGG AGCCCACCC 2050

GGTCACGCTG GCCACAGCAC AAAGAACAAAC TCCTCACCAAG TTCATCCTGA 2100

25 GGCTGGGAGG ACCGGGATGC TGGATTCTGT TTTCCGAAGT CACTGCAGCG 2150

GATGATGGAA CTGAATCGAT ACGGTGTTT CTGTCCCTCC TACTTCCTT 2200

30 CACACCAGAC AGCCCCTCAT GTCTCCAGGA CAGGACAGGA CTACAGACAA 2250

CTCTTTCTTT AAATAAATTA AGTCTCTACA ATAAAAAAA 2290

(2) INFORMATION FOR SEQ ID NO:2:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Pro Leu Cys Val Thr Cys Trp Trp Leu Gly Leu Leu Ala
1 5 10 15

5 Ala Met Gly Ala Val Ala Gly Gln Glu Asp Gly Phe Glu Gly Thr
20 25 30

Glu Glu Gly Ser Pro Arg Glu Phe Ile Tyr Leu Asn Arg Tyr Lys
10 35 40 45

Arg Ala Gly Glu Ser Gln Asp Lys Cys Thr Tyr Thr Phe Ile Val
50 55 60

15 Pro Gln Gln Arg Val Thr Gly Ala Ile Cys Val Asn Ser Lys Glu
65 70 75

Pro Glu Val Leu Leu Glu Asn Arg Val His Lys Gln Glu Leu Glu
20 80 85 90

Leu Leu Asn Asn Glu Leu Leu Lys Gln Lys Arg Gln Ile Glu Thr
95 100 105

25 Leu Gln Gln Leu Val Glu Val Asp Gly Gly Ile Val Ser Glu Val
110 115 120

Lys Leu Leu Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr
125 130 135

30 Gln Leu Tyr Met Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp
140 145 150

Asn Ala Leu Glu Leu Ser Gln Leu Glu Asn Arg Ile Leu Asn Gln
155 160 165

35 Thr Ala Asp Met Leu Gln Leu Ala Ser Lys Tyr Lys Asp Leu Glu
170 175 180

PATENT DOCKET P1130

His Lys Tyr Gln His Leu Ala Thr Leu Ala His Asn Gln Ser Glu
185 190 195

Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro Ser Ala
5 200 205 210

Arg Pro Val Pro Gln Pro Pro Pro Ala Ala Pro Pro Arg Val Tyr
215 220 225

10 Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn
230 235 240

Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu
245 250 255

15 Pro Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys
260 265 270

20 Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly
275 280 285

His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn
290 295 300

25 Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly
305 310 315

Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe
320 325 330

30 Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly
335 340 345

35 Glu Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln
350 355 360

PATENT DOCKET P1130

Gly Asn Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg
365 370 375

Lys Val Phe Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser
5 380 385 390

Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly
395 400 405

Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe Thr Thr Leu Asp
10 410 415 420

Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His Tyr Gln Lys
425 430 435

Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu Asn Gly
15 440 445 450

Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp Gly
20 455 460 465

Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys
470 475 480

25 Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
485 490 493

(2) INFORMATION FOR SEQ ID NO:3:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3355 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

PATENT DOCKET P1130

GCAGCTGGTT ACTGCATTC TCCATGTGGC AGACAGAGCA AAGCCACAAC 50

GCTTCTCTG CTGGATTAAA GACGGCCCAC AGACCAGAAC TTCCACTATA 100

5 CTACTTAAAA TTACATAGGT GGCTTGTCAA ATTCAATTGA TTAGTATTGT 150

AAAAGGAAAA AGAAGTCCT TCTTACAGCT TGGATTCAAC GGTCCAAAAC 200

10 AAAAATGCAG CTGCCATTAA AGTCTCAGAT GAACAAACTT CTACACTGAT 250

TTTAAAATC AAGAATAAGG GCAGCAAGTT TCTGGATTCA CTGAATCAAC 300

AGACACAAAA AGCTGGCAAT ATAGCAACTA TGAAGAGAAA AGCTACTAAT 350

15 AAAATTAACC CAACGCATAG AAGACTTTT TTTCTCTTCT AAAAACAACT 400

AAGTAAAGAC TTAAATTAA ACACATCATT TTACAACCTC ATTTCAAAAT 450

20 GAAGACTTTT ACCTGGACCC TAGGTGTGCT ATTCTTCCTA CTAGTGGACA 500

CTGGACATTG CAGAGGTGGA CAATTCAAAA TTAAAAAAAT AAACCAGAGA 550

AGATACCCTC GTGCCACAGA TGGTAAAGAG GAAGCAAAGA AATGTGCATA 600

25 CACATTCTG GTACCTGAAC AAAGAATAAC AGGGCCAATC TGTGTCAACA 650

CCAAGGGGCA AGATGCAAGT ACCATTAAAG ACATGATCAC CAGGATGGAC 700

CTTGAAAACC TGAAGGATGT GCTCTCCAGG CAGAAGCGGG AGATAGATGT 750

30 TCTGCAACTG GTGGTGGATG TAGATGGAAA CATTGTGAAT GAGGTAAAGC 800

TGCTGAGAAA GGAAAGCCGT AACATGAACT CTCGTGTTAC TCAACTCTAT 850

35 ATGCAATTAT TACATGAGAT TATCCGTAAG AGGGATAATT CACTTGAACT 900

TTCCCAACTG GAAAACAAAA TCCTCAATGT CACCACAGAA ATGTTGAAGA 950

PATENT DOCKET P1130

TGGCAACAAG ATACAGGGAA CTAGAGGTGA AATACGCTTC CTTGACTGAT 1000

CTTGTCAATA ACCAATCTGT GATGATCACT TTGTTGGAAG AACAGTGCTT 1050

5 GAGGATATTT TCCCGACAAG ACACCCATGT GTCTCCCCA CTTGTCCAGG 1100

TGGTGCCACA ACATATTCTT AACAGCCAAC AGTATACTCC TGGTCTGCTG 1150

10 GGAGGTAACG AGATTCAAGG GGATCCAGGT TATCCCAGAG ATTTAATGCC 1200

ACCACCTGAT CTGGCAACTT CTCCCCACAA AAGCCCTTC AAGATACCAC 1250

CGGTAACCTT CATCAATGAA GGACCATTCA AAGACTGTCA GCAAGCAAAA 1300

15 GAAGCTGGGC ATTGGTCAG TGGGATTAT ATGATTAAC CTGAAACAG 1350

CAATGGACCA ATGCAGTTAT GGTGTGAAAA CAGTTGGAC CCTGGGGTT 1400

GGACTGTTAT TCAGAAAAGA ACAGACGGCT CTGTCAACTT CTTCAGAAAT 1450

20 TGGGAAAATT ATAAGAAAGG GTTTGGAAC ATTGACGGAG AATACTGGCT 1500

TGGACTGGAA AATATCTATA TGCTTAGCAA TCAAGATAAT TACAAGTTAT 1550

25 TGATTGAATT AGAAGACTGG AGTGATAAAA AAGTCTATGC AGAATACAGC 1600

AGCTTCGTC TGGAACCTGA AAGTGAATTC TATAGACTGC GCCTGGGAAC 1650

TTACCAGGGA AATGCAGGGG ATTCTATGAT GTGGCATAAT GGTAAACAAT 1700

30 TCACCACACT GGACAGAGAT AAAGATATGT ATGCAGGAAA CTGCGCCCAC 1750

TTTCATAAAG GAGGCTGGTG GTACAATGCC TGTGCACATT CTAACCTAAA 1800

35 TGGAGTATGG TACAGAGGAG GCCATTACAG AAGCAAGCAC CAAGATGGAA 1850

TTTTCTGGGC CGAATACAGA GGCAGGTCAT ACTCCTTAAG AGCAGTTCA 1900

PATENT DOCKET P1130

ATGATGATCA AGCCTATTGA CTGAAGAGAG ACACCTGCCA ATTTAAATGA 1950

CACAGAACTT TGTACTTTTC AGCTCTTAAA AATGTAAATG TTACATGTAT 2000

5 ATTACTTGGC ACAATTATT TCTACACAGA AAGTTTTAA AATGAATT 2050

ACCGTAACTA TAAAAGGGAA CCTATAATG TAGTTTCATC TGCGTCAAT 2100

TACTGCAGAA AATTATGTGT ATCCACAACC TAGTTATTAA AAAAATTATG 2150

10 TTGACTAAAT ACAAAAGTTG TTTTCTAAAA TGTAAATATT TGCCACAATG 2200

TAAAGCAAAT CTTAGCTATA TTTAAATCA TAAATAACAT GTTCAAGATA 2250

15 CTTAACAAATT TATTAAAAT CTAAGATTGC TCTAACGTCT AGTAAAAAAA 2300

ATATTTTTA AATTCAGCC AAATAATGCA TTTTATTAA TAAAATACA 2350

GACAGAAAAT TAGGGAGAAA CTTCTAGTT TGCCAATAGA AAATGTTCTT 2400

20 CCATTGAATA AAAGTTATT CAAATTGAAT TTGTGCCTTT CACACGTAAT 2450

GATTAAATCT GAATTCTAA TAATATATCC TATGCTGATT TTCCCAAAAC 2500

25 ATGACCCATA GTATTAAATA CATATCATTT TTAAAAATAA AAAAAAACCC 2550

AAAAATAATG CATGCATAAT TTAAATGGTC AATTTATAAA GACAAATCTA 2600

TGAATGAATT TTTCAGTGT ATCTTCATAT GATATGCTGA ACACCAAAAT 2650

30 CTCCAGAAAT GCATTTATG TAGTTCTAAA ATCAGCAAAA TATTGGTATT 2700

ACAAAAATGC AGAATATTAA GTGTGCTACA GATCTGAATT ATAGTTCTAA 2750

35 TTTATTATTA CTTTTTTCT AATTTACTGA TCTTACTACT ACAAAAGAAAA 2800

AAAAACCCAA CCCATCTGCA ATTCAAATCA GAAAGTTGG ACAGCTTAC 2850

AAGTATTAGT GCATGCTCAG AACAGGTGGG ACTAAAACAA ACTCAAGGAA 2900

CTGTTGGCTG TTTTCCCGAT ACTGAGAATT CAACAGCTCC AGAGCAGAAG 2950

5 CCACAGGGGC ATAGCTTAGT CCAAACGTCT AATTCATTT TACAGTGTAT 3000

GTAACGCTTA GTCTCACAGT GTCTTTACT CATCTTGCA ATCAACAACT 3050

TTACTAGTGA CTTTCTGGAA CAATTCCTT TCAGGAATAC ATATTCACTG 3100

10 CTTAGAGGTG ACCTTGCCTT AATATATTG TGAAGTTAAA ATTTTAAAGA 3150

TAGCTCATGA AACTTTGCT TAAGCAAAAA GAAAACCTCG AATTGAAATG 3200

15 TGTGAGGCAA ACTATGCATG GGAATAGCTT AATGTGAAGA TAATCATTG 3250

GACAACCTCAA ATCCATCAAC ATGACCAATG TTTTCATCT GCCACATCTC 3300

AAAATAAAAC TTCTGGTGAA ACAAAATTAAA CAAAATATCC AAACCTCAAA 3350

20 AAAAAA 3355

(2) INFORMATION FOR SEQ ID NO:4:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Thr Phe Thr Trp Thr Leu Gly Val Leu Phe Phe Leu Leu
1 5 10 15

35 Val Asp Thr Gly His Cys Arg Gly Gly Gln Phe Lys Ile Lys Lys
20 25 30

PATENT DOCKET P1130

Ile Asn Gln Arg Arg Tyr Pro Arg Ala Thr Asp Gly Lys Glu Glu
35 40 45

5 Ala Lys Lys Cys Ala Tyr Thr Phe Leu Val Pro Glu Gln Arg Ile
50 55 60

Thr Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr
65 70 75

10 Ile Lys Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp
80 85 90

Val Leu Ser Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val
95 100 105

15 Val Asp Val Asp Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg
110 115 120

20 Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met
125 130 135

Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn Ser Leu Glu
140 145 150

25 Leu Ser Gln Leu Glu Asn Lys Ile Leu Asn Val Thr Thr Glu Met
155 160 165

Leu Lys Met Ala Thr Arg Tyr Arg Glu Leu Glu Val Lys Tyr Ala
170 175 180

30 Ser Leu Thr Asp Leu Val Asn Asn Gln Ser Val Met Ile Thr Leu
185 190 195

35 Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser Arg Gln Asp Thr His
200 205 210

PATENT DOCKET P1130

Val Ser Pro Pro Leu Val Gln Val Val Pro Gln His Ile Pro Asn
215 220 225

Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn Glu Ile Gln
5 230 235 240

Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro Asp Leu
245 250 255

Ala Thr Ser Pro Thr Lys Ser Pro Phe Lys Ile Pro Pro Val Thr
10 260 265 270

Phe Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys Glu
275 280 285

Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
15 290 295 300

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro
20 305 310 315

Gly Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn
25 320 325 330

Phe Phe Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile
335 340 345

Asp Gly Glu Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser
30 350 355 360

Asn Gln Asp Asn Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser
365 370 375

Asp Lys Lys Val Tyr Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro
35 380 385 390

PATENT DOCKET P1130

Glu Ser Glu Phe Tyr Arg Leu Arg Leu Gly Thr Tyr Gln Gly Asn
395 400 405

Ala Gly Asp Ser Met Met Trp His Asn Gly Lys Gln Phe Thr Thr
5 410 415 420

Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn Cys Ala His Phe
425 430 435

His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
10 440 445 450

Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys His Gln
455 460 465

Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly Ser Tyr Ser Leu
15 470 475 480

Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
20 485 490 491

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1780 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCTCAGAGG CCCCACTGGA CCCTCGGCTC TTCCCTGGAC TTCTTGTGTG 50

35 TTCTGTGAGC TTCGCTGGAT TCAGGGTCTT GGGCATCAGA GGTGAGAGGG 100

TGGGAAGGTC CGCCGCGATG GGGAAAGCCCT GGCTGCGTGC GCTACAGCTG 150

PATENT DOCKET P1130

CTGCTCCTGC TGGGCGCGTC GTGGGCGCGG GCGGGCGCCC CGCGCTGCAC 200

CTACACCTTC GTGCTGCCCC CGCAGAAGTT CACGGGCGCT GTGTGCTGGA 250

5 GCGGCCCGC ATCCACGCGG GCGACGCCCG AGGCCGCCAA CGCCAGCGAG 300

CTGGCGGCCGC TGCGCATGCG CGTCGGCCGC CACGAGGAGC TGTTACGCGA 350

GCTGCAGAGG CTGGCGCGG CCGACGGCGC CGTGGCCGGC GAGGTGCGCG 400

10 CGCTGCGCAA GGAGAGCCGC GGCCTGAGCG CGCGCCTGGG CCAGTTGCGC 450

GCGCAGCTGC AGCACGAGGC GGGGCCCGGG GCGGGCCCGG GGGCGGATCT 500

15 GGGGGCGGAG CCTGCCGCGG CGCTGGCGCT GCTCGGGGAG CGCGTGCTCA 550

ACCGTCCGC CGAGGCTCAG CGCGCAGCCG CCCGGTTCCA CCAGCTGGAC 600

GTCAAGTTCC GCGAGCTGGC GCAGCTCGTC ACCCAGCAGA GCAGTCTCAT 650

20 CGCCCGCCTG GAGCGCCTGT GCCCGGGAGG CGCGGGCGGG CAGCAGCAGG 700

TCCTGCCGCC ACCCCCCACTG GTGCCTGTGG TTCCGGTCCG TCTTGTGGGT 750

25 AGCACCAGTG ACACCAGTAG GATGCTGGAC CCAGCCCCAG AGCCCCAGAG 800

AGACCAGACC CAGAGACAGC AGGAGCCCAT GGCTTCTCCC ATGCCTGCAG 850

GTCACCCCTGC GGTCCCCACC AAGCCTGTGG GCCCGTGGCA GGATTGTGCA 900

30 GAGGCCCGCC AGGCAGGCCA TGAACAGAGT GGAGTGTATG AACTGCGAGT 950

GGGCCGTAC GTAGTGTAC TATGGTGTGA GCAGCAACTG GAGGGTGGAG 1000

35 GCTGGACTGT GATCCAGCGG AGGCAAGATG GTTCAGTCAA CTTCTTCACT 1050

ACCTGGCAGC ACTATAAGGC GGGCTTGGG CGGCCAGACG GAGAATACTG 1100

PATENT DOCKET P1130

GCTGGGCCTT GAACCCGTGT ATCAGCTGAC CAGCCGTGGG GACCATGAGC 1150

TGCTGGTTCT CCTGGAGGAC TGGGGGGGCC GTGGAGCAGC TGCCCACAT 1200

5 GATGGCTTCT CCCTGGAACC CGAGAGCGAC CACTACCGCC TGC GGCTTGG 1250

CCAGTACCAT GGTGATGCTG GAGACTCTCT TTCCTGGCAC AATGACAAGC 1300

CCTTCAGCAC CGTGGATAGG GACCGAGACT CCTATTCTGG TAACTGTGCC 1350

10 CTGTACCAGC GGGGAGGCTG GTGGTACCAT GCCTGTGCC ACTCCAACCT 1400

CAACGGTGTG TGGCACCAACG GCGGCCACTA CCGAAGCCGC TACCAGGATG 1450

15 GTGTCTACTG GGCTGAGTTT CGTGGTGGGG CATATTCTCT CAGGAAGGCC 1500

GCCATGCTCA TTCGGCCCT GAAGCTGTGA CTCTGTGTTCTCTGTCCCC 1550

TAGGCCCTAG AGGACATTGG TCAGCAGGAG CCCAAGTTGT TCTGGCCACA 1600

20 CCTTCTTGTT GGCTCAGTGC CAATGTGTCC CACAGAACTT CCCACTGTGG 1650

ATCTGTGACC CTGGCGCTG AAAATGGGAC CCAGGAATCC CCCCCGTCAA 1700

25 TATCTTGGCC TCAGATGGCT CCCCAAGGTC ATTCAATATCT CGGTTTGAGC 1750

TCATATCTTA TAATAACACA AAGTAGGCCAC 1780

(2) INFORMATION FOR SEQ ID NO:6:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Lys Pro Trp Leu Arg Ala Leu Gln Leu Leu Leu Leu
1 5 10 15

Gly Ala Ser Trp Ala Arg Ala Gly Ala Pro Arg Cys Thr Tyr Thr
20 25 30

Phe Val Leu Pro Pro Gln Lys Phe Thr Gly Ala Val Cys Trp Ser
10 35 40 45

Gly Pro Ala Ser Thr Arg Ala Thr Pro Glu Ala Ala Asn Ala Ser
50 55 60

Glu Leu Ala Ala Leu Arg Met Arg Val Gly Arg His Glu Glu Leu
15 65 70 75

Leu Arg Glu Leu Gln Arg Leu Ala Ala Ala Asp Gly Ala Val Ala
20 80 85 90

Gly Glu Val Arg Ala Leu Arg Lys Glu Ser Arg Gly Leu Ser Ala
25 95 100 105

Arg Leu Gly Gln Leu Arg Ala Gln Leu Gln His Glu Ala Gly Pro
110 115 120

Gly Ala Gly Pro Gly Ala Asp Leu Gly Ala Glu Pro Ala Ala Ala
125 130 135

Leu Ala Leu Leu Gly Glu Arg Val Leu Asn Ala Ser Ala Glu Ala
30 140 145 150

Gln Arg Ala Ala Ala Arg Phe His Gln Leu Asp Val Lys Phe Arg
155 160 165

Glu Leu Ala Gln Leu Val Thr Gln Gln Ser Ser Leu Ile Ala Arg
35 170 175 180

PATENT DOCKET P1130

Leu Glu Arg Leu Cys Pro Gly Gly Ala Gly Gly Gln Gln Val
185 190 195

5 Leu Pro Pro Pro Leu Val Pro Val Val Pro Val Arg Leu Val
200 205 210

Gly Ser Thr Ser Asp Thr Ser Arg Met Leu Asp Pro Ala Pro Glu
215 220 225

10 Pro Gln Arg Asp Gln Thr Gln Arg Gln Gln Glu Pro Met Ala Ser
230 235 240

Pro Met Pro Ala Gly His Pro Ala Val Pro Thr Lys Pro Val Gly
245 250 255

15 Pro Trp Gln Asp Cys Ala Glu Ala Arg Gln Ala Gly His Glu Gln
260 265 270

Ser Gly Val Tyr Glu Leu Arg Val Gly Arg His Val Val Ser Val
275 280 285

20 Trp Cys Glu Gln Gln Leu Glu Gly Gly Trp Thr Val Ile Gln
290 295 300

25 Arg Arg Gln Asp Gly Ser Val Asn Phe Phe Thr Thr Trp Gln His
305 310 315

Tyr Lys Ala Gly Phe Gly Arg Pro Asp Gly Glu Tyr Trp Leu Gly
320 325 330

30 Leu Glu Pro Val Tyr Gln Leu Thr Ser Arg Gly Asp His Glu Leu
335 340 345

35 Leu Val Leu Leu Glu Asp Trp Gly Gly Arg Gly Ala Arg Ala His
350 355 360

PATENT DOCKET P1130

Tyr Asp Gly Phe Ser Leu Glu Pro Glu Ser Asp His Tyr Arg Leu
365 370 375

Arg Leu Gly Gln Tyr His Gly Asp Ala Gly Asp Ser Leu Ser Trp
5 380 385 390

His Asn Asp Lys Pro Phe Ser Thr Val Asp Arg Asp Arg Asp Ser
395 400 405

10 Tyr Ser Gly Asn Cys Ala Leu Tyr Gln Arg Gly Gly Trp Trp Tyr
410 415 420

His Ala Cys Ala His Ser Asn Leu Asn Gly Val Trp His His Gly
425 430 435

15 Gly His Tyr Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu
440 445 450

20 Phe Arg Gly Gly Ala Tyr Ser Leu Arg Lys Ala Ala Met Leu Ile
455 460 465

Arg Pro Leu Lys Leu
470

25 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: Nucleic Acid
- 30 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTGACGAAC CAAGGCAACT ACAAACTCCT GGT 33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10

TGC GGCC GGA CCAGTCCTCC ATGGTCACCA GGAGTTTGTA G 41

(2) INFORMATION FOR SEQ ID NO:9:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

25

GGTGGTGAAC TGCTTGCCGT TGTGCCATGT AAA 33

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGTTATCC CAGAGATTAA ATGCCACCA 29

(2) INFORMATION FOR SEQ ID NO:11:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTGGTGGGAG AAGTTGCCAG ATCAGGTGGT GGCA 34

15

(2) INFORMATION FOR SEQ ID NO:12:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCACACCAT AACTGCATTG GTCCA 25

30 (2) INFORMATION FOR SEQ ID NO:13:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGTAGTTCC AGTATGGTGT GAGCAGCAAC TGGA 34

(2) INFORMATION FOR SEQ ID NO:14:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

15

AGTCCAGCCT CCACCCTCCA GTTGCT 26

(2) INFORMATION FOR SEQ ID NO:15:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCAGTCCT CCAGGAGAAC CAGCA 25

30

(2) INFORMATION FOR SEQ ID NO:16:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2042 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GC GGACGCGT GGGTGAAATT GAAAATCAAG ATAAAAATGT TCACAATTAA 50

5

GCTCCTTCTT TTTATTGTTC CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100

ACAATTCAATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTGCT 150

10

ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200

TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250

TTCAAAAATC CAACATATTG GATCAGTCTT TTTATGATCT ATCGCTGCAA 300

15

ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350

ACTACAAGTC AAAATGAAG AGGTAAAGAA TATGTCACTT GAACTCAACT 400

20

CAAAACTTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450

AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500

TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTGTA GAAAACAAG 550

25

ATAATAGCAT CAAAGACCTT CTCCAGACCG TGGAAGACCA ATATAAACAA 600

TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650

30

GACTAGTATT CAAGAACCCA CAGAAATTTC TCTATCTTCC AAGCCAAGAG 700

CACCAAGAAC TACTCCCTT CTTCAGTTGA ATGAAATAAG AAATGTAAAA 750

CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800

35

TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTCATG 850

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TCTACTGTGA TGTTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900

ATAGATGGAT CACAAAACCTT CAATGAAACG TGGGAGAACT ACAAAATATGG 950

5 TTTTGGGAGG CTTGATGGAG AATTTGGTT GGGCCTAGAG AAGATATACT 1000

CCATAGTGAA GCAATCTAAT TATGTTTAC GAATTGAGTT GGAAGACTGG 1050

AAAGACAACA AACATTATAT TGAATATTCT TTTTACCTGG GAAATCACGA 1100

10 AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCCAATG 1150

CAATCCCGGA AAACAAAGAT TTGGTGTTCCTACTTGGGA TCACAAAGCA 1200

15 AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250

TGATGAGTGT GGAGAAAACA ACCTAAATGG TAAATATAAC AAACCAAGAG 1300

20 CAAAATCTAA GCCAGAGAGG AGAAGAGGAT TATCTTGGAA GTCTAAAAT 1350

GGAAGGTTAT ACTCTATAAA ATCAACCAAA ATGTTGATCC ATCCAACAGA 1400

TTCAGAAAGC TTTGAATGAA CTGAGGCAAT TTAAAGGCAT ATTTAACCAT 1450

25 TAACTCATTC CAAGTTAATG TGGTCTAATA ATCTGGTATA AATCCTTAAG 1500

AGAAAGCTTG AGAAATAGAT TTTTTTATC TTAAAGTCAC TGTCTATTAA 1550

AGATTAAACA TACAATCACA TAACCTTAAA GAATACCGTT TACATTCTC 1600

30 AATCAAATT CTTATAATAC TATTTGTTT AAATTTGTG ATGTGGGAAT 1650

CAATTTAGA TGGTCACAAT CTAGATTATA ATCAATAGGT GAACTTATTA 1700

35 AATAACTTTT CTAAATAAAA AATTTAGAGA CTTTTATTTT AAAAGGCATC 1750

ATATGAGCTA ATATCACAAAC TTTCCCAGTT TAAAAAACTA GTACTCTGT 1800

TAAAACCTCTA AACTTGACTA AATACAGAGG ACTGGTAATT GTACAGTTCT 1850

TAAATGTTGT AGTATTAATT TCAAAACTAA AAATCGTCAG CACAGAGTAT 1900

5 GTGTAAAAAT CTGTAATACA AATTTTAAA CTGATGCTTC ATTTGCTAC 1950

AAAATAATT GGAGTAAATG TTTGATATGA TTTATTTATG AACCTAATG 2000

AAGCAGAATT AAATACTGTA TTAAAATAAG TTCGCTGTCT TT 2042

10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Phe Thr Ile Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile

1 5 10 15

Ser Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser

20 25 30

Pro Glu Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile

35 40 45

Leu Ala Asn Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe

30 50 55 60

Val His Lys Thr Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu

65 70 75

Asn Ile Phe Asp Gln Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser

35 80 85 90

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Glu Ile Lys Glu Glu Glu Lys Glu Leu Arg Arg Thr Thr Tyr Lys
95 100 105

5 Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met Ser Leu Glu Leu
110 115 120

Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile Leu Leu Gln
125 130 135

10 Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu Ile Gln
140 145 150

Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu Lys
155 160 165

15 Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln
170 175 180

20 Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln
185 190 195

Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu
200 205 210

25 Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr
215 220 225

Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp
230 235 240

30 Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His
245 250 255

35 Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe
260 265 270

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His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile
275 280 285

Gln His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu
5 290 295 300

Asn Tyr Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu
305 310 315

Gly Leu Glu Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val
10 320 325 330

Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile
335 340 345

Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr Asn Tyr Thr Leu
15 350 355 360

His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala Ile Pro Glu
20 365 370 375

Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala Lys Gly
25 380 385 390

His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp His
395 400 405

Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro
30 410 415 420

Arg Ala Lys Ser Lys Pro Glu Arg Arg Gly Leu Ser Trp Lys
425 430 435

Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu
35 440 445 450

Ile His Pro Thr Asp Ser Glu Ser Phe Glu
455 460